

SEQUENCE LISTING

<110> JENAPHARM GmbH & Co. KG															
<120> Methods for Determining Hormonal Effects of Substances															
<130> Pat 3684/11															
<140> US/10/791,017															
<141> 2004-03-02															
<160> 8															
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Met Ala Ser Thr															
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Asp Tyr Ser Thr Tyr Ser Gln Ala Ala Ala Gln Gln Gly Tyr Ser Ala															
5 10 15 20															
tac acc gcc cag ccc act caa gga tat gca cag acc acc cag gca tat														151	
Tyr Thr Ala Gln Pro Thr Gln Gly Tyr Ala Gln Thr Thr Gln Ala Tyr															
25 30 35															
ggg caa caa agc tat gga acc tat gga cag ccc act gat gtc agc tat														199	
Gly Gln Gln Ser Tyr Gly Thr Tyr Gly Gln Pro Thr Asp Val Ser Tyr															
40 45 50															
acc cag gct cag acc act gca acc tat ggg cag acc gcc tat gca act														247	
Thr Gln Ala Gln Thr Thr Ala Thr Tyr Gly Gln Thr Ala Tyr Ala Thr															
55 60 65															
tct tat gga cag cct ccc act ggt tat act act cca act gcc ccc cag														295	
Ser Tyr Gly Gln Pro Pro Thr Gly Tyr Thr Thr Pro Thr Ala Pro Gln															
70 75 80															
gca tac agc cag cct gtc cag ggg tat ggc act ggt gct tat gat acc														343	
Ala Tyr Ser Gln Pro Val Gln Gly Tyr Gly Thr Gly Ala Tyr Asp Thr															
85 90 95 100															
acc act gct aca gtc acc acc acc cag gcc tcc tat gca gct cag tct														391	
Thr Thr Ala Thr Val Thr Thr Thr Gln Ala Ser Tyr Ala Ala Gln Ser															
105 110 115															
gca tat ggc act cag cct gct tat cca gcc tat ggg cag cag cca gca														439	
Ala Tyr Gly Thr Gln Pro Ala Tyr Pro Ala Tyr Gly Gln Gln Pro Ala															
120 125 130															
gcc act gca cct aca aga ccg cag gat gga aac aag ccc act gag act														487	
Ala Thr Ala Pro Thr Arg Pro Gln Asp Gly Asn Lys Pro Thr Glu Thr															

135	140	145	
agt caa cct caa tct agc aca ggg ggt tac aac cag ccc agc cta gga Ser Gln Pro Gln Ser Ser Thr Gly Gly Tyr Asn Gln Pro Ser Leu Gly 150 155 160			535
tat gga cag agt aac tac agt tat ccc cag gta cct ggg agc tac ccc Tyr Gly Gln Ser Asn Tyr Ser Tyr Pro Gln Val Pro Gly Ser Tyr Pro 165 170 175 180			583
atg cag cca gtc act gca cct cca tcc tac cct cct acc agc tat tcc Met Gln Pro Val Thr Ala Pro Pro Ser Tyr Pro Pro Thr Ser Tyr Ser 185 190 195			631
tct aca cag ccg act agt tat gat cag agc agt tac tct cag cag aac Ser Thr Gln Pro Thr Ser Tyr Asp Gln Ser Ser Tyr Ser Gln Gln Asn 200 205 210			679
acc tat ggg caa ccg agc agc tat gga cag cag agt agc tat ggt caa Thr Tyr Gly Gln Pro Ser Ser Tyr Gly Gln Gln Ser Ser Tyr Gly Gln 215 220 225			727
caa agc agc tat ggg cag cag cct ccc act agt tac cca ccc caa act Gln Ser Ser Tyr Gly Gln Gln Pro Pro Thr Ser Tyr Pro Pro Gln Thr 230 235 240			775
gga tcc tac agc caa gct cca agt caa tat agc caa cag agc agc agc Gly Ser Tyr Ser Gln Ala Pro Ser Gln Tyr Ser Gln Gln Ser Ser Ser 245 250 255 260			823
tac ggg cag cag agt tca ttc cga cag gac cac ccc agt agc atg ggt Tyr Gly Gln Gln Ser Ser Phe Arg Gln Asp His Pro Ser Ser Met Gly 265 270 275			871
gtt tat ggg cag gag tct gga gga ttt tcc gga cca gga gag aac cgg Val Tyr Gly Gln Glu Ser Gly Gly Phe Ser Gly Pro Gly Glu Asn Arg 280 285 290			919
agc atg agt ggc cct gat aac cgg ggc agg gga aga ggg gga ttt gat Ser Met Ser Gly Pro Asp Asn Arg Gly Arg Gly Arg Gly Gly Phe Asp 295 300 305			967
cgt gga ggc atg agc aga ggt ggg cgg gga gga gga cgc ggt gga atg Arg Gly Gly Met Ser Arg Gly Gly Arg Gly Gly Arg Gly Gly Met 310 315 320			1015
ggc agc gct gga gag cga ggt ggc ttc aat aag cct ggt gga ccc atg Gly Ser Ala Gly Glu Arg Gly Gly Phe Asn Lys Pro Gly Gly Pro Met 325 330 335 340			1063
gat gaa gga cca gat ctt gat cta ggc cca cct gta gat cca gat gaa Asp Glu Gly Pro Asp Leu Asp Leu Gly Pro Pro Val Asp Pro Asp Glu 345 350 355			1111
gac tct gac aac agt gca att tat gta caa gga tta aat gac agt gtg Asp Ser Asp Asn Ser Ala Ile Tyr Val Gln Gly Leu Asn Asp Ser Val 360 365 370			1159

act cta gat gat ctg gca gac ttc ttt aag cag tgt ggg gtt gtt aag	1207
Thr Leu Asp Asp Leu Ala Asp Phe Phe Lys Gln Cys Gly Val Val Lys	
375 380 385	
atg aac aag aga act ggg caa ccc atg atc cac atc tac ctg gac aag	1255
Met Asn Lys Arg Thr Gly Gln Pro Met Ile His Ile Tyr Leu Asp Lys	
390 395 400	
gaa aca gga aag ccc aaa ggc gat gcc aca gtg tcc tat gaa gac cca	1303
Glu Thr Gly Lys Pro Lys Gly Asp Ala Thr Val Ser Tyr Glu Asp Pro	
405 410 415 420	
ccc act gcc aag gct gcc gtg gaa tgg ttt gat ggg aaa gat ttt caa	1351
Pro Thr Ala Lys Ala Ala Val Glu Trp Phe Asp Gly Lys Asp Phe Gln	
425 430 435	
ggg agc aaa ctt aaa gtc tcc ctt gct cgg aag aag cct cca atg aac	1399
Gly Ser Lys Leu Lys Val Ser Leu Ala Arg Lys Lys Pro Pro Met Asn	
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agt atg cgg ggt ggt ctg cca ccc cgt gag ggc aga ggc atg cca cca	1447
Ser Met Arg Gly Gly Leu Pro Pro Arg Glu Gly Arg Gly Met Pro Pro	
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cca ctc cgt gga ggt cca gga ggc cca gga ggt cct ggg gga ccc atg	1495
Pro Leu Arg Gly Gly Pro Gly Gly Pro Gly Gly Pro Gly Gly Pro Met	
470 475 480	
ggt cgc atg gga ggc cgt gga gga gat aga gga ggc ttc cct cca aga	1543
Gly Arg Met Gly Gly Arg Gly Gly Asp Arg Gly Gly Phe Pro Pro Arg	
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gga ccc cgg ggt tcc cga ggg aac ccc tct gga gga gga aac gtc cag	1591
Gly Pro Arg Gly Ser Arg Gly Asn Pro Ser Gly Gly Gly Asn Val Gln	
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cac cga gct gga gac tgg cag tgt ccc aat ccg ggt tgt gga aac cag	1639
His Arg Ala Gly Asp Trp Gln Cys Pro Asn Pro Gly Cys Gly Asn Gln	
520 525 530	
aac ttc gcc tgg aga aca gag tgc aac cag tgt aag gcc cca aag cct	1687
Asn Phe Ala Trp Arg Thr Glu Cys Asn Gln Cys Lys Ala Pro Lys Pro	
535 540 545	
gaa ggc ttc ctc ccg cca ccc ttt ccg ccc ccg ggt ggt gat cgt ggc	1735
Glu Gly Phe Leu Pro Pro Pro Phe Pro Pro Pro Gly Gly Asp Arg Gly	
550 555 560	
aga ggt ggc cct ggt ggc atg cgg gga gga aga ggt ggc ctc atg gat	1783
Arg Gly Gly Pro Gly Gly Met Arg Gly Gly Arg Gly Gly Leu Met Asp	
565 570 575 580	
cgt ggt ggt ccc ggt gga atg ttc aga ggt ggc cgt ggt gga gac aga	1831
Arg Gly Gly Pro Gly Gly Met Phe Arg Gly Gly Arg Gly Gly Asp Arg	
585 590 595	

ggt ggc ttc cgt ggt ggc cgg ggc atg gac cga ggt ggc ttt ggt gga 1879
 Gly Gly Phe Arg Gly Gly Arg Gly Met Asp Arg Gly Gly Phe Gly Gly
 600 605 610

gga aga cga ggt ggc cct ggg ggg ccc cct gga cct ttg atg gaa cag 1927
 Gly Arg Arg Gly Gly Pro Gly Gly Pro Pro Gly Pro Leu Met Glu Gln
 615 620 625

atg gga gga aga aga gga gga cgt gga gga cct gga aaa atg gat aaa 1975
 Met Gly Gly Arg Arg Gly Gly Arg Gly Gly Pro Gly Lys Met Asp Lys
 630 635 640

ggc gag cac cgt cag gag cgc aga gat cgg ccc tac tagatgcaga 2021
 Gly Glu His Arg Gln Glu Arg Arg Asp Arg Pro Tyr
 645 650 655

gaccccgag agctgcattg actaccagat ttatttttta aaccagaaaa tgtttttaaat 2081

ttataattcc atattttataa tgttggccac aacattatga ttattccttg tctgtacttt 2141

agtatttttc accattttgtg aagaaacatt aaaacaagtt aaatggtagt gtgcggagtt 2201

tttttttctt ccttcctttta aaaatggttg tttaagactt taacaatggg aacccttgt 2261

gagcatgctc agtatcattg tggagaacca agagggcctc ttaactgtaa caatgttcat 2321

ggttgtgatg tttttttttt ttttttaaaa taaattcca aatgtttaat aaaaaaaaaa 2381

aaaaaaaaa 2390

<210> 2

<211> 656

<212> PRT

<213> Homo sapiens

<400> 2

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Thr Gln Ala Tyr Gly Gln Gln Ser Tyr Gly Thr Tyr Gly Gln Pro Thr
 35 40 45

Asp Val Ser Tyr Thr Gln Ala Gln Thr Thr Ala Thr Tyr Gly Gln Thr
 50 55 60

Ala Tyr Ala Thr Ser Tyr Gly Gln Pro Pro Thr Gly Tyr Thr Thr Pro
 65 70 75 80

Thr Ala Pro Gln Ala Tyr Ser Gln Pro Val Gln Gly Tyr Gly Thr Gly
 85 90 95

Ala Tyr Asp Thr Thr Thr Ala Thr Val Thr Thr Thr Gln Ala Ser Tyr
 100 105 110
 Ala Ala Gln Ser Ala Tyr Gly Thr Gln Pro Ala Tyr Pro Ala Tyr Gly
 115 120 125
 Gln Gln Pro Ala Ala Thr Ala Pro Thr Arg Pro Gln Asp Gly Asn Lys
 130 135 140
 Pro Thr Glu Thr Ser Gln Pro Gln Ser Ser Thr Gly Gly Tyr Asn Gln
 145 150 155 160
 Pro Ser Leu Gly Tyr Gly Gln Ser Asn Tyr Ser Tyr Pro Gln Val Pro
 165 170 175
 Gly Ser Tyr Pro Met Gln Pro Val Thr Ala Pro Pro Ser Tyr Pro Pro
 180 185 190
 Thr Ser Tyr Ser Ser Thr Gln Pro Thr Ser Tyr Asp Gln Ser Ser Tyr
 195 200 205
 Ser Gln Gln Asn Thr Tyr Gly Gln Pro Ser Ser Tyr Gly Gln Gln Ser
 210 215 220
 Ser Tyr Gly Gln Gln Ser Ser Tyr Gly Gln Gln Pro Pro Thr Ser Tyr
 225 230 235 240
 Pro Pro Gln Thr Gly Ser Tyr Ser Gln Ala Pro Ser Gln Tyr Ser Gln
 245 250 255
 Gln Ser Ser Ser Tyr Gly Gln Gln Ser Ser Phe Arg Gln Asp His Pro
 260 265 270
 Ser Ser Met Gly Val Tyr Gly Gln Glu Ser Gly Gly Phe Ser Gly Pro
 275 280 285
 Gly Glu Asn Arg Ser Met Ser Gly Pro Asp Asn Arg Gly Arg Gly Arg
 290 295 300
 Gly Gly Phe Asp Arg Gly Gly Met Ser Arg Gly Gly Arg Gly Gly Gly
 305 310 315 320
 Arg Gly Gly Met Gly Ser Ala Gly Glu Arg Gly Gly Phe Asn Lys Pro
 325 330 335
 Gly Gly Pro Met Asp Glu Gly Pro Asp Leu Asp Leu Gly Pro Pro Val
 340 345 350
 Asp Pro Asp Glu Asp Ser Asp Asn Ser Ala Ile Tyr Val Gln Gly Leu
 355 360 365
 Asn Asp Ser Val Thr Leu Asp Asp Leu Ala Asp Phe Phe Lys Gln Cys
 370 375 380
 Gly Val Val Lys Met Asn Lys Arg Thr Gly Gln Pro Met Ile His Ile
 385 390 395 400

Tyr Leu Asp Lys Glu Thr Gly Lys Pro Lys Gly Asp Ala Thr Val Ser
405 410 415

Tyr Glu Asp Pro Pro Thr Ala Lys Ala Ala Val Glu Trp Phe Asp Gly
420 425 430

Lys Asp Phe Gln Gly Ser Lys Leu Lys Val Ser Leu Ala Arg Lys Lys
435 440 445

Pro Pro Met Asn Ser Met Arg Gly Gly Leu Pro Pro Arg Glu Gly Arg
450 455 460

Gly Met Pro Pro Pro Leu Arg Gly Gly Pro Gly Gly Pro Gly Gly Pro
465 470 475 480

Gly Gly Pro Met Gly Arg Met Gly Gly Arg Gly Gly Asp Arg Gly Gly
485 490 495

Phe Pro Pro Arg Gly Pro Arg Gly Ser Arg Gly Asn Pro Ser Gly Gly
500 505 510

Gly Asn Val Gln His Arg Ala Gly Asp Trp Gln Cys Pro Asn Pro Gly
515 520 525

Cys Gly Asn Gln Asn Phe Ala Trp Arg Thr Glu Cys Asn Gln Cys Lys
530 535 540

Ala Pro Lys Pro Glu Gly Phe Leu Pro Pro Pro Phe Pro Pro Pro Gly
545 550 555 560

Gly Asp Arg Gly Arg Gly Gly Pro Gly Gly Met Arg Gly Gly Arg Gly
565 570 575

Gly Leu Met Asp Arg Gly Gly Pro Gly Gly Met Phe Arg Gly Gly Arg
580 585 590

Gly Gly Asp Arg Gly Gly Phe Arg Gly Gly Arg Gly Met Asp Arg Gly
595 600 605

Gly Phe Gly Gly Gly Arg Arg Gly Gly Pro Gly Gly Pro Pro Gly Pro
610 615 620

Leu Met Glu Gln Met Gly Gly Arg Arg Gly Gly Arg Gly Gly Pro Gly
625 630 635 640

Lys Met Asp Lys Gly Glu His Arg Gln Glu Arg Arg Asp Arg Pro Tyr
645 650 655

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<211> 20

<212> DNA

<213> artificial sequence

<220>

<223> Primer

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<210> 4
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<212> DNA
<213> artificial sequence

<220>
<223> Primer

<400> 4
gttgaagtga acttggcggg g 21

<210> 5
<211> 27
<212> DNA
<213> artificial sequence

<220>
<223> Primer

<400> 5
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<210> 6
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<212> DNA
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<220>
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<212> DNA
<213> artificial sequence

<220>
<223> Primer

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<211> 918
<212> PRT
<213> Homo sapiens

<400> 8

Met Glu Val Gln Leu Gly Leu Gly Arg Val Tyr Pro Arg Pro Pro Ser
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Lys Thr Tyr Arg Gly Ala Phe Gln Asn Leu Phe Gln Ser Val Arg Glu
20 25 30
Val Ile Gln Asn Pro Gly Pro Arg His Pro Glu Ala Ala Ser Ala Ala
35 40 45
Pro Pro Gly Ala Ser Leu Leu Leu Leu Gln Gln Gln Gln Gln Gln
50 55 60
Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Glu Thr Ser Pro Arg Gln
65 70 75 80
Gln Gln Gln Gln Gln Gln Glu Asp Gly Ser Pro Gln Ala His Arg Arg
85 90 95
Gly Pro Thr Gly Tyr Leu Val Leu Asp Glu Glu Gln Gln Pro Ser Gln
100 105 110
Pro Gln Ser Ala Leu Glu Cys His Pro Glu Arg Gly Cys Val Pro Glu
115 120 125
Pro Gly Ala Ala Val Ala Ala Ser Lys Gly Leu Pro Gln Gln Leu Pro
130 135 140
Ala Pro Pro Asp Glu Asp Asp Ser Ala Ala Pro Ser Thr Leu Ser Leu
145 150 155 160
Leu Gly Pro Thr Phe Pro Gly Leu Ser Ser Cys Ser Ala Asp Leu Lys
165 170 175
Asp Ile Leu Ser Glu Ala Ser Thr Met Gln Leu Leu Gln Gln Gln Gln
180 185 190
Gln Glu Ala Val Ser Glu Gly Ser Ser Ser Gly Arg Ala Arg Glu Ala
195 200 205
Ser Gly Ala Pro Thr Ser Ser Lys Asp Asn Tyr Leu Gly Gly Thr Ser
210 215 220
Thr Ile Ser Asp Asn Ala Lys Glu Leu Cys Lys Ala Val Ser Val Ser
225 230 235 240
Met Gly Leu Gly Val Glu Ala Leu Glu His Leu Ser Pro Gly Glu Gln
245 250 255
Leu Arg Gly Asp Cys Met Tyr Ala Pro Leu Leu Gly Val Pro Pro Ala
260 265 270
Val Arg Pro Thr Pro Cys Ala Pro Leu Ala Glu Cys Lys Gly Ser Leu
275 280 285

Leu Asp Asp Ser Ala Gly Lys Ser Thr Glu Asp Thr Ala Glu Tyr Ser
290 295 300

Pro Phe Lys Gly Gly Tyr Thr Lys Gly Leu Glu Gly Glu Ser Leu Gly
305 310 315 320

Cys Ser Gly Ser Ala Ala Ala Gly Ser Ser Gly Thr Leu Glu Leu Pro
325 330 335

Ser Thr Leu Ser Leu Tyr Lys Ser Gly Ala Leu Asp Glu Ala Ala Ala
340 345 350

Tyr Gln Ser Arg Asp Tyr Tyr Asn Phe Pro Leu Ala Leu Ala Gly Pro
355 360 365

Pro Pro Pro Pro Pro Pro Pro His Pro His Ala Arg Ile Lys Leu Glu
370 375 380

Asn Pro Leu Asp Tyr Gly Ser Ala Trp Ala Ala Ala Ala Ala Gln Cys
385 390 395 400

Arg Tyr Gly Asp Leu Ala Ser Leu His Gly Ala Gly Ala Ala Gly Pro
405 410 415

Gly Ser Gly Ser Pro Ser Ala Ala Ala Ser Ser Ser Trp His Thr Leu
420 425 430

Phe Thr Ala Glu Glu Gly Gln Leu Tyr Gly Pro Cys Gly Gly Gly Gly
435 440 445

Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
450 455 460

Gly Gly Gly Gly Gly Gly Gly Gly Glu Ala Glu Ala Val Ala Pro Tyr Gly
465 470 475 480

Tyr Thr Arg Pro Pro Gln Gly Leu Ala Gly Gln Glu Ser Asp Phe Thr
485 490 495

Ala Pro Asp Val Trp Tyr Pro Gly Gly Met Val Ser Arg Val Pro Tyr
500 505 510

Pro Ser Pro Thr Cys Val Lys Ser Glu Met Gly Pro Trp Met Asp Ser
515 520 525

Tyr Ser Gly Pro Tyr Gly Asp Met Arg Leu Glu Thr Ala Arg Asp His
530 535 540

Val Leu Pro Ile Asp Tyr Tyr Phe Pro Pro Gln Lys Thr Cys Leu Ile
545 550 555 560

Cys Gly Asp Glu Ala Ser Gly Cys His Tyr Gly Ala Leu Thr Cys Gly
565 570 575

Ser Cys Lys Val Phe Phe Lys Arg Ala Ala Glu Gly Lys Gln Lys Tyr
580 585 590

Leu Cys Ala Ser Arg Asn Asp Cys Thr Ile Asp Lys Phe Arg Arg Lys
 595 600 605
 Asn Cys Pro Ser Cys Arg Leu Arg Lys Cys Tyr Glu Ala Gly Met Thr
 610 615 620
 Leu Gly Ala Arg Lys Leu Lys Lys Leu Gly Asn Leu Lys Leu Gln Glu
 625 630 635 640
 Glu Gly Glu Ala Ser Ser Thr Thr Ser Pro Thr Glu Glu Thr Thr Gln
 645 650 655
 Lys Leu Thr Val Ser His Ile Glu Gly Tyr Glu Cys Gln Pro Ile Phe
 660 665 670
 Leu Asn Val Leu Glu Ala Ile Glu Pro Gly Val Val Cys Ala Gly His
 675 680 685
 Asp Asn Asn Gln Pro Asp Ser Phe Ala Ala Leu Leu Ser Ser Leu Asn
 690 695 700
 Glu Leu Gly Glu Arg Gln Leu Val His Val Val Lys Trp Ala Lys Ala
 705 710 715 720
 Leu Pro Gly Phe Arg Asn Leu His Val Asp Asp Gln Met Ala Val Ile
 725 730 735
 Gln Tyr Ser Trp Met Gly Leu Met Val Phe Ala Met Gly Trp Arg Ser
 740 745 750
 Phe Thr Asn Val Asn Ser Arg Met Leu Tyr Phe Ala Pro Asp Leu Val
 755 760 765
 Phe Asn Glu Tyr Arg Met His Lys Ser Arg Met Tyr Ser Gln Cys Val
 770 775 780
 Arg Met Arg His Leu Ser Gln Glu Phe Gly Trp Leu Gln Ile Thr Pro
 785 790 795 800
 Gln Glu Phe Leu Cys Met Lys Ala Leu Leu Leu Phe Ser Ile Ile Pro
 805 810 815
 Val Asp Glu Leu Arg Met Asn Tyr Ile Lys Glu Leu Asp Arg Met Asn
 820 825 830
 Tyr Ile Lys Leu Glu Asp Arg Ile Ile Ala Cys Lys Arg Lys Asn Pro
 835 840 845
 Thr Ser Cys Ser Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Ser
 850 855 860
 Val Gln Pro Ile Ala Arg Glu Leu His Gln Phe Thr Phe Asp Leu Leu
 865 870 875 880
 Ile Lys Ser His Met Val Ser Val Asp Phe Pro Glu Met Met Ala Glu
 885 890 895

Ile Ile Ser Val Gln Val Pro Lys Ile Leu Ser Gly Lys Val Lys Pro
900 905 910

Ile Tyr Phe His Thr Gln
915